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1/45

SEQUENCE LISTING

<110> CHUGAI SEIYAKU KABUSHIKI KAISHA
IRIE, Reiko

<120> IgM PRODUCTION BY TRANSFORMED CELL AND
METHOD OF QUANTIFYING THE SAME

<130> C1-A0223P

<150> US 60/487,333

<151> 2003-07-15

<160> 31

<170> PatentIn version 3.1

<210> 1

<211> 1779

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1779)

<223>

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Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly

1 5 10 15

gtc cag tgt gag gtg cag ctg ttg gat tct ggg gga ggc ttg gta cag 96

Val Gln Cys Glu Val Gln Leu Leu Asp Ser Gly Gly Gly Leu Val Gln

20 25 30

cct ggg ggg tgc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt 144

Pro Gly Gly Cys Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe

35 40 45

agc agc tgt gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg 192

Ser Ser Cys Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu

50 55 60

gag tgg gtc tca gct att agt ggt agt ggt ggt agc aca tac tac gca 240

Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala

65 70 75 80

gac tcc gtg aag ggc cgg ttc acc atc tcc aga gac aaa tcc aag aac 288

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Lys Asn

85 90 95

acg ttg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gta	336
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val	
100 105 110	
tat tac tgt gcg aaa ggt ggc aac gat att ttg act ggt tat tat gct	384
Tyr Tyr Cys Ala Lys Gly Gly Asn Asp Ile Leu Thr Gly Tyr Tyr Ala	
115 120 125	
tgg ggc cag gga acc ctg gtc acc gtc tcc tca ggg agt gca tcc gcc	432
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Ala Ser Ala	
130 135 140	
cca acc ctt ttc ccc ctc gtc tcc tgt gag aat tcc ccg tcg gat acg	480
Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro Ser Asp Thr	
145 150 155 160	
agc agc gtg gcc gtt ggc tgc ctc gca cag gac ttc ctt ccc gac tcc	528
Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu Pro Asp Ser	
165 170 175	
atc act ttc tcc tgg aaa tac aag aac aac tct gac atc agc agc acc	576
Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile Ser Ser Thr	
180 185 190	
cgg ggc ttc cca tca gtc ctg aga ggg ggc aag tac gca gcc acc tca	624
Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys Tyr Ala Ala Thr Ser	

195	200	205	
cag gtg ctg ctg cct tcc aag gac gtc atg cag ggc aca gac gaa cac			672
Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr Asp Glu His			
210	215	220	
gtg gtg tgc aaa gtc cag cac ccc aac ggc aac aaa gaa aag aac gtg			720
Val Val Cys Lys Val Gln His Pro Asn Gly Asn Lys Glu Lys Asn Val			
225	230	235	240
cct ctt cca gtg att gct gag ctg cct ccc aaa gtg agc gtc ttc gtc			768
Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val			
245	250	255	
cca ccc cgc gac ggc ttc ttc ggc aac ccc cgc aag tcc aag ctc atc			816
Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile			
260	265	270	
tgc cag gcc acg ggt ttc agt ccc cgg cag att cag gtg tcc tgg ctg			864
Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp Leu			
275	280	285	
cgc gag ggg aag cag gtg ggg tct ggc gtc acc acg gac cag gtg cag			912
Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln			
290	295	300	

gct gag gcc aaa gag tct ggg ccc acg acc tac aag gtg acc agc aca 960
Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr
305 310 315 320

ctg acc atc aaa gag agc gac tgg ctc ggc cag agc atg ttc acc tgc 1008
Leu Thr Ile Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr Cys
325 330 335

cgc gtg gat cac agg ggc ctg acc ttc cag cag aat gcg tcc tcc atg 1056
Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met
340 345 350

tgt gtc ccc gat caa gac aca gcc atc cgg gtc ttc gcc atc ccc cca 1104
Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile Pro Pro
355 360 365

tcc ttt gcc agc atc ttc ctc acc aag tcc acc aag ttg acc tgc ctg 1152
Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu
370 375 380

gtc aca gac ctg acc acc tat gac agc gtg acc atc tcc tgg acc cgc 1200
Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg
385 390 395 400

cag aat ggc gaa gct gtg aaa acc cac acc aac atc tcc gag agc cac 1248
Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu Ser His

6/45

405	410	415	
ccc aat gcc act ttc agc gcc gtg ggt gag gcc agc atc tgc gag gat			1296
Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys Glu Asp			
420	425	430	
gac tgg aat tcc ggg gag agg ttc acg tgc acc gtg acc cac aca gac			1344
Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp			
435	440	445	
ctg ccc tcg cca ctg aag cag acc atc tcc cgg ccc aag ggg gtg gcc			1392
Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly Val Ala			
450	455	460	
ctg cac agg ccc gat gtc tac ttg ctg cca cca gcc cgg gag cag ctg			1440
Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg Glu Gln Leu			
465	470	475	480
aac ctg cgg gag tcg gcc acc atc acg tgc ctg gtg acg ggc ttc tct			1488
Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr Gly Phe Ser			
485	490	495	
ccc gcg gac gtc ttc gtg cag tgg atg cag agg ggg cag ccc ttg tcc			1536
Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln Pro Leu Ser			
500	505	510	

ccg gag aag tat gtg acc agc gcc cca atg cct gag ccc cag gcc cca 1584

Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro Gln Ala Pro

515

520

525

ggc cgg tac ttc gcc cac agc atc ctg acc gtg tcc gaa gag gaa tgg 1632

Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu Glu Glu Trp

530

535

540

aac acg ggg gag acc tac acc tgc gtg gtg gcc cat gag gcc ctg ccc 1680

Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu Ala Leu Pro

545

550

555

560

aac agg gtc acc gag agg acc gtg gac aag tcc acc ggt aaa ccc acc 1728

Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly Lys Pro Thr

565

570

575

ctg tac aac gtg tcc ctg gtc atg tcc gac aca gct ggc acc tgc tac 1776

Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly Thr Cys Tyr

580

585

590

tga

1779

<210> 2

<211> 592

<212> PRT

<213> Homo sapiens

<400> 2

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Val Gln Cys Glu Val Gln Leu Leu Asp Ser Gly Gly Gly Leu Val Gln

20 25 30

Pro Gly Gly Cys Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe

35 40 45

Ser Ser Cys Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu

50 55 60

Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala

65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Lys Asn

85 90 95

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val

100 105 110

Tyr Tyr Cys Ala Lys Gly Gly Asn Asp Ile Leu Thr Gly Tyr Tyr Ala

115 120 125

9/45

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Ala Ser Ala

130

135

140

Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro Ser Asp Thr

145

150

155

160

Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu Pro Asp Ser

165

170

175

Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile Ser Ser Thr

180

185

190

Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys Tyr Ala Ala Thr Ser

195

200

205

Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr Asp Glu His

210

215

220

Val Val Cys Lys Val Gln His Pro Asn Gly Asn Lys Glu Lys Asn Val

225

230

235

240

Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val

245

250

255

Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile

260

265

270

10/45

Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp Leu

275

280

285

Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln

290

295

300

Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr

305

310

315

320

Leu Thr Ile Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr Cys

325

330

335

Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met

340

345

350

Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile Pro Pro

355

360

365

Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu

370

375

380

Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg

385

390

395

400

Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu Ser His

11/45

405

410

415

Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys Glu Asp

420

425

430

Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp

435

440

445

Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly Val Ala

450

455

460

Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg Glu Gln Leu

465

470

475

480

Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr Gly Phe Ser

485

490

495

Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln Pro Leu Ser

500

505

510

Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro Gln Ala Pro

515

520

525

Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu Glu Glu Trp

530

535

540

12/45

Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu Ala Leu Pro

545 550 555 560

Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly Lys Pro Thr

565 570 575

Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly Thr Cys Tyr

580 585 590

<210> 3

<211> 723

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1).. (723)

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Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser

1 5 10 15

ggt gcc tac ggg gac atc gtg atg acc cag tct cca gac tcc ctg gct 96

Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala

13/45

20	25	30	
gtg tct ctg ggc gag agg gcc acc atc aac tgc aag tcc agc cag agt 144			
Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser			
35	40	45	
gtt tta tac agc tcc aac aat aag aac tac tta gct tgg tac cag cag 192			
Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln			
50	55	60	
aaa cca gga cag cct cct aag ctg ctc att tac tgg gca tct acc cgg 240			
Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg			
65	70	75	80
gaa tcc ggg gtc cct gac cga ttc agt ggc agc ggg tct ggg aca gat 288			
Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp			
85	90	95	
ttc act ctc acc atc agc agc ctg cag gct gaa gat gtg gca gtt tat 336			
Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr			
100	105	110	
tac tgt cag caa tat tat agt act cct ccg acg ttc ggc caa ggg acc 384			
Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr			
115	120	125	

aag gtg gaa atc aaa cga act gtg gct gca cca tct gtc ttc atc ttc 432

Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe

130

135

140

ccg cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc 480

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys

145

150

155

160

ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg 528

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val

165

170

175

gat aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag 576

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln

180

185

190

gac agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc 624

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser

195

200

205

aaa gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat 672

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His

210

215

220

cag ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt 720

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys

15/45

225

230

235

240

tag

723

<210> 4

<211> 240

<212> PRT

<213> Homo sapiens

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Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala

20

25

30

Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser

35

40

45

Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln

50

55

60

Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg

65

70

75

80

Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp

16/45

85

90

95

Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr

100

105

110

Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr

115

120

125

Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe

130

135

140

Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys

145

150

155

160

Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val

165

170

175

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln

180

185

190

Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser

195

200

205

Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His

210

215

220

Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys

225 230 235 240

<210> 5

<211> 480

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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Met Lys Asn His Leu Leu Phe Trp Gly Val Leu Ala Val Phe Ile Lys

1 5 10 15

gct gtt cat gtg aaa gcc caa gaa gat gaa agg att gtt ctt gtt gac 96

Ala Val His Val Lys Ala Gln Glu Asp Glu Arg Ile Val Leu Val Asp

20 25 30

aac aaa tgt aag tgt gcc cgg att act tcc agg atc atc cgt tct tcc 144

Asn Lys Cys Lys Cys Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser

35 40 45

gaa gat cct aat gag gac att gtg gag aga aac atc cga att att gtt 192

Glu Asp Pro Asn Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile Val

50

55

60

cct ctg aac aac agg gag aat atc tct gat ccc acc tca cca ttg aga 240

Pro Leu Asn Asn Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg

65

70

75

80

acc aga ttt gtg tac cat ttg tct gac ctc tgt aaa aaa tgt gat cct 288

Thr Arg Phe Val Tyr His Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro

85

90

95

aca gaa gtg gag ctg gat aat cag ata gtt act gct acc cag agc aat 336

Thr Glu Val Glu Leu Asp Asn Gln Ile Val Thr Ala Thr Gln Ser Asn

100

105

110

atc tgt gat gaa gac agt gct aca gag acc tgc tac act tat gac aga 384

Ile Cys Asp Glu Asp Ser Ala Thr Glu Thr Cys Tyr Thr Tyr Asp Arg

115

120

125

aac aag tgc tac aca gct gtg gtc cca ctc gta tat ggt ggt gag acc 432

Asn Lys Cys Tyr Thr Ala Val Val Pro Leu Val Tyr Gly Gly Glu Thr

130

135

140

aaa atg gtg gaa aca gcc tta acc cca gat gcc tgc tat cct gac taa 480

Lys Met Val Glu Thr Ala Leu Thr Pro Asp Ala Cys Tyr Pro Asp

19/45

145

150

155

<210> 6

<211> 159

<212> PRT

<213> Homo sapiens

<400> 6

Met Lys Asn His Leu Leu Phe Trp Gly Val Leu Ala Val Phe Ile Lys

1

5

10

15

Ala Val His Val Lys Ala Gln Glu Asp Glu Arg Ile Val Leu Val Asp

20

25

30

Asn Lys Cys Lys Cys Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser

35

40

45

Glu Asp Pro Asn Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile Val

50

55

60

Pro Leu Asn Asn Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg

65

70

75

80

Thr Arg Phe Val Tyr His Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro

85

90

95

20/45

Thr Glu Val Glu Leu Asp Asn Gln Ile Val Thr Ala Thr Gln Ser Asn

100

105

110

Ile Cys Asp Glu Asp Ser Ala Thr Glu Thr Cys Tyr Thr Tyr Asp Arg

115

120

125

Asn Lys Cys Tyr Thr Ala Val Val Pro Leu Val Tyr Gly Gly Glu Thr

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Lys Met Val Glu Thr Ala Leu Thr Pro Asp Ala Cys Tyr Pro Asp

145

150

155

<210> 7

<211> 24

<212> DNA

<213> Artificial

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<223> an artificially synthesized sequence

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ccaacggcaa caaagaaaag aacg

24

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<211> 24

<212> DNA

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<223> an artificially synthesized sequence

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aacatgctct ggccgagcca gtcg

24

<210> 9

<211> 24

<212> DNA

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gcaagtcag ccagagtgtt ttat

24

<210> 10

<211> 24

<212> DNA

<213> Artificial

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ctgtccttgc tgtcctgctc tgtg

24

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<211> 33

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<223> an artificially synthesized primer sequence

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<210> 12

<211> 32

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<213> Artificial

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agcggccagc cgccccgagc ctgtcgacag gc

32

<210> 13

<211> 32

<212> DNA

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<400> 13

atagaattcc accatggtgt tgcagacca gg

32

<210> 14

<211> 30

<212> DNA

<213> Artificial

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ggagcaggcg gccgcacttc tccctctaac

30

<210> 15

<211> 24

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized sequence

<400> 15

accattgaga accagatttg tgta

24

<210> 16

<211> 24

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized sequence

<400> 16

tgtgtagcac ttgtttctgt cata

24

<210> 17

<211> 28

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 17

atgaattcca ccatgaagaa ccatttgc

28

<210> 18

<211> 26

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 18

tatctagatt agtcaggata gcaggc

26

<210> 19

<211> 1788

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1).. (1788)

<223>

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48

26/45

Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly

1 5 10 15

gtc cag tgt gag gtg cag ctg ttg gag tct ggg gga ggc ttg gta cag 96

Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln

20 25 30

ccg ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt 144

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe

35 40 45

agc agc tat gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg 192

Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu

50 55 60

gag tgg gtc tca gct att agt ggt agt ggt tat acc aca tac tac gca 240

Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Tyr Thr Thr Tyr Tyr Ala

65 70 75 80

gac tcc gtg aag ggc cgg ttc acc atc tcc aga gac aat tcc aag aac 288

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn

85 90 95

acg ctg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gta 336

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val

100 105 110

tat tac tgt gcc aaa aaa ccg ggg gac tat ggt tgc ggg agt tat tac 384
 Tyr Tyr Cys Ala Lys Lys Pro Gly Asp Tyr Gly Ser Gly Ser Tyr Tyr
 115 120 125

ctt gac tac tgg ggc cag gga acc ctg gtc acc gtc tcc tca ggg agt 432
 Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser
 130 135 140

gca tcc gcc cca acc ctt ttc ccc ctc gtc tcc tgt gag aat tcc ccg 480
 Ala Ser Ala Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro
 145 150 155 160

tgc gat acg agc agc gtg gcc gtt ggc tgc ctc gca cag gac ttc ctt 528
 Ser Asp Thr Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu
 165 170 175

ccc gac tcc atc act ttc tcc tgg aaa tac aag aac aac tct gac atc 576
 Pro Asp Ser Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile
 180 185 190

agc agc acc cgg ggc ttc cca tca gtc ctg aga ggg ggc aag tac gca 624
 Ser Ser Thr Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys Tyr Ala
 195 200 205

gcc acc tca cag gtg ctg ctg cct tcc aag gac gtc atg cag ggc aca 672

Ala Thr Ser Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr

210

215

220

gac gaa cac gtg gtg tgc aaa gtc cag cac ccc aac ggc aac aaa gaa 720

Asp Glu His Val Val Cys Lys Val Gln His Pro Asn Gly Asn Lys Glu

225

230

235

240

aag aac gtg cct ctt cca gtg att gct gag ctg cct ccc aaa gtg agc 768

Lys Asn Val Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys Val Ser

245

250

255

gtc ttc gtc cca ccc cgc gac ggc ttc ttc ggc aac ccc cgc aag tcc 816

Val Phe Val Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser

260

265

270

aag ctc atc tgc cag gcc acg ggt ttc agt ccc cgg cag att cag gtg 864

Lys Leu Ile Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val

275

280

285

tcc tgg ctg cgc gag ggg aag cag gtg ggg tct ggc gtc acc acg gac 912

Ser Trp Leu Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp

290

295

300

cag gtg cag gct gag gcc aaa gag tct ggg ccc acg acc tac aag gtg 960

Gln Val Gln Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val

305

310

315

320

acc agc aca ctg acc atc aaa gag agc gac tgg ctc agc cag agc atg 1008
 Thr Ser Thr Leu Thr Ile Lys Glu Ser Asp Trp Leu Ser Gln Ser Met
 325 330 335

ttc acc tgc cgc gtg gat cac agg ggc ctg acc ttc cag cag aat gcg 1056
 Phe Thr Cys Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala
 340 345 350

tcc tcc atg tgt gtc ccc gat caa gac aca gcc atc cgg gtc ttc gcc 1104
 Ser Ser Met Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala
 355 360 365

atc ccc cca tcc ttt gcc agc atc ttc ctc acc aag tcc acc aag ttg 1152
 Ile Pro Pro Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu
 370 375 380

acc tgc ctg gtc aca gac ctg acc acc tat gac agc gtg acc atc tcc 1200
 Thr Cys Leu Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser
 385 390 395 400

tgg acc cgc cag aat ggc gaa gct gtg aaa acc cac acc aac atc tcc 1248
 Trp Thr Arg Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser
 405 410 415

gag agc cac ccc aat gcc act ttc agc gcc gtg ggt gag gcc agc atc 1296

Glu Ser His Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile

420

425

430

tgc gag gat gac tgg aat tcc ggg gag agg ttc acg tgc acc gtg acc 1344

Cys Glu Asp Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr

435

440

445

cac aca gac ctg ccc tcg cca ctg aag cag acc atc tcc cgg ccc aag 1392

His Thr Asp Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys

450

455

460

ggg gtg gcc ctg cac agg ccc gat gtc tac ttg ctg cca cca gcc cgg 1440

Gly Val Ala Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg

465

470

475

480

gag cag ctg aac ctg cgg gag tcg gcc acc atc acg tgc ctg gtg acg 1488

Glu Gln Leu Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr

485

490

495

ggc ttc tct ccc gcg gac gtc ttc gtg cag tgg atg cag agg ggg cag 1536

Gly Phe Ser Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln

500

505

510

ccc ttg tcc ccg gag aag tat gtg acc agc gcc cca atg cct gag ccc 1584

Pro Leu Ser Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro

515

520

525

cag gcc cca ggc cgg tac ttc gcc cac agc atc ctg acc gtg tcc gaa 1632

Gln Ala Pro Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu

530

535

540

gag gaa tgg aac acg ggg gag acc tac acc tgc gtg gtg gcc cat gag 1680

Glu Glu Trp Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu

545

550

555

560

gcc ctg ccc aac agg gtc acc gag agg acc gtg gac aag tcc acc ggt 1728

Ala Leu Pro Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly

565

570

575

aaa ccc acc ctg tac aac gtg tcc ctg gtc atg tcc gac aca gct ggc 1776

Lys Pro Thr Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly

580

585

590

acc tgc tac tga

1788

Thr Cys Tyr

595

<210> 20

<211> 595

<212> PRT

<213> Homo sapiens

<400> 20

Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly

1

5

10

15

Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln

20

25

30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe

35

40

45

Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu

50

55

60

Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Tyr Thr Thr Tyr Tyr Ala

65

70

75

80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn

85

90

95

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val

100

105

110

Tyr Tyr Cys Ala Lys Lys Pro Gly Asp Tyr Gly Ser Gly Ser Tyr Tyr

115

120

125

Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser

130

135

140

Ala Ser Ala Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro

145

150

155

160

Ser Asp Thr Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu

165

170

175

Pro Asp Ser Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile

180

185

190

Ser Ser Thr Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys Tyr Ala

195

200

205

Ala Thr Ser Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr

210

215

220

Asp Glu His Val Val Cys Lys Val Gln His Pro Asn Gly Asn Lys Glu

225

230

235

240

Lys Asn Val Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys Val Ser

245

250

255

Val Phe Val Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser

260

265

270

34/45

Lys Leu Ile Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val

275

280

285

Ser Trp Leu Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp

290

295

300

Gln Val Gln Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val

305

310

315

320

Thr Ser Thr Leu Thr Ile Lys Glu Ser Asp Trp Leu Ser Gln Ser Met

325

330

335

Phe Thr Cys Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala

340

345

350

Ser Ser Met Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala

355

360

365

Ile Pro Pro Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu

370

375

380

Thr Cys Leu Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser

385

390

395

400

Trp Thr Arg Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser

405

410

415

Glu Ser His Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile
420 425 430

Cys Glu Asp Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr
435 440 445

His Thr Asp Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys
450 455 460

Gly Val Ala Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg
465 470 475 480

Glu Gln Leu Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr
485 490 495

Gly Phe Ser Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln
500 505 510

Pro Leu Ser Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro
515 520 525

Gln Ala Pro Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu
530 535 540

Glu Glu Trp Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu

545

550

555

560

Ala Leu Pro Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly

565

570

575

Lys Pro Thr Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly

580

585

590

Thr Cys Tyr

595

<210> 21

<211> 726

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1).. (726)

<223>

<400> 21

atg gtg ttg cag acc cag gtc ttc att tct ctg ttg ctc tgg atc tct

48

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser

1

5

10

15

ggt gcc tac ggg gac atc gtg atg acc cag tct cca gac tcc ctg gct 96

Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala

20

25

30

gtg tct ctg ggc gag agg gcc acc atc aac tgc aag tcc agc cag agt 144

Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser

35

40

45

gtt tta tac agc tcc aac aat aag aac tac tta gct tgg tac cag cag 192

Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln

50

55

60

aaa cca gga cag cct cct aag ttg ctc att tac tgg gca tct acc cgg 240

Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg

65

70

75

80

gaa tcc ggg gtc cct gac cga ttc agt ggc agc ggg tct ggg aca gat 288

Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp

85

90

95

ttc act ctc acc atc agc agc ctg cag gct gaa gat gtg gca gtt tat 336

Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr

100

105

110

tac tgt cag caa tat tat act act ctt ccg ctc act ttc ggc gga ggg 384

Tyr Cys Gln Gln Tyr Tyr Thr Thr Leu Pro Leu Thr Phe Gly Gly Gly

115	120	125	
acc aag gtg gag atc aaa cga act gtg gct gca cca tct gtc ttc atc			432
Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile			
130	135	140	
ttc ccg cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg			480
Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val			
145	150	155	160
tgc ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag			528
Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys			
	165	170	175
gtg gat aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag			576
Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu			
	180	185	190
cag gac agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg			624
Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu			
195	200	205	
agc aaa gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc			672
Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr			
210	215	220	

39/45

cat cag ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag 720

His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu

225 230 235 240

tgt tag

726

Cys

<210> 22

<211> 241

<212> PRT

<213> Homo sapiens

<400> 22

Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser

1 5 10 15

Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala

20 25 30

Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser

35 40 45

Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln

50 55 60

Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg

65

70

75

80

Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp

85

90

95

Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr

100

105

110

Tyr Cys Gln Gln Tyr Tyr Thr Thr Leu Pro Leu Thr Phe Gly Gly Gly

115

120

125

Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile

130

135

140

Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val

145

150

155

160

Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys

165

170

175

Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu

180

185

190

Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu

195

200

205

Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr

210

215

220

His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu

225

230

235

240

Cys

<210> 23

<211> 24

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 23

caacaggcag gcaggggcag caag

24

<210> 24

<211> 24

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 24

agcataatta aagccaagga ggag

24

<210> 25

<211> 68

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized sequence

<400> 25

cctgatcatg aagacgtcga ctagtccgga tccccgggag ctcgagcgct ctagatcttt

60

aattaagg

68

<210> 26

<211> 76

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized sequence

<400> 26

cgcgcccttaa tttaaagatct agagcgctcg agctcccggg gatccggact agtcgacgtc 60

ttcatgatca ggccgg

76

<210> 27

<211> 23

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 27

gaggaattcc accatgaaga acc

23

<210> 28

<211> 27

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 28

gaggcggccg ctagtcagg atagcag

27

<210> 29

<211> 32

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 29

aaaagcggcc gcgatcataa tcagccatac ca

32

<210> 30

<211> 36

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized primer sequence

<400> 30

aaaactcgag aagcttagac atgataagat acattg

36

<210> 31

<211> 12

<212> DNA

<213> Artificial

<220>

<223> an artificially synthesized linker sequence

<400> 31

cccggatccg gg